



## SEQUENCE LISTING

<110> Wolfman, Neil  
Bouxsein, Mary

<120> ActRIIB Fusion Polypeptides and Uses Therefor

<130> 08702.0093-00000

<140> US 10/689,677

<141> 2003-10-22

<150> US 60/421,041

<151> 2002-10-25

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 512

<212> PRT

<213> Human

<400> 1

Met Thr Ala Pro Trp Val Ala Leu Ala Leu Leu Trp Gly Ser Leu Cys  
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Ala Gly Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu Cys Ile Tyr Tyr  
20 25 30

Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser Gly Leu Glu Arg  
35 40 45

Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr Ala Ser Trp Ala  
50 55 60

Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly Cys Trp Leu Asp  
65 70 75 80

Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala Thr Glu Glu Asn  
85 90 95

Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe Cys Asn Glu Arg  
100 105 110

Phe Thr His Leu Pro Glu Ala Gly Gly Pro Glu Val Thr Tyr Glu Pro  
115 120 125

Pro Pro Thr Ala Pro Thr Leu Leu Thr Val Leu Ala Tyr Ser Leu Leu  
130 135 140

Pro Ile Gly Gly Leu Ser Leu Ile Val Leu Leu Ala Phe Trp Met Tyr  
145 150 155 160

Arg His Arg Lys Pro Pro Tyr Gly His Val Asp Ile His Glu Asp Pro  
165 170 175

Gly Pro Pro Pro Ser Pro Leu Val Gly Leu Lys Pro Leu Gln Leu  
180 185 190

Leu Glu Ile Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys Ala Gln  
195 200 205

Leu Met Asn Asp Phe Val Ala Val Lys Ile Phe Pro Leu Gln Asp Lys  
210 215 220

Gln Ser Trp Gln Ser Glu Arg Glu Ile Phe Ser Thr Pro Gly Met Lys  
225 230 235 240

His Glu Asn Leu Leu Gln Phe Ile Ala Ala Glu Lys Arg Gly Ser Asn  
245 250 255

Leu Glu Val Glu Leu Trp Leu Ile Thr Ala Phe His Asp Lys Gly Ser  
260 265 270

Leu Thr Asp Tyr Leu Lys Gly Asn Ile Ile Thr Trp Asn Glu Leu Cys  
275 280 285

His Val Ala Glu Thr Met Ser Arg Gly Leu Ser Tyr Leu His Glu Asp  
290 295 300

Val Pro Trp Cys Arg Gly Glu Gly His Lys Pro Ser Ile Ala His Arg  
305 310 315 320

Asp Phe Lys Ser Lys Asn Val Leu Leu Lys Ser Asp Leu Thr Ala Val  
325 330 335

Leu Ala Asp Phe Gly Leu Ala Val Arg Phe Glu Pro Gly Lys Pro Pro  
340 345 350

Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro Glu  
355 360 365

Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg Ile  
370 375 380

Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Val Ser Arg Cys  
385 390 395 400

Lys Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu Glu  
405 410 415

Glu Ile Gly Gln His Pro Ser Leu Glu Glu Leu Gln Glu Val Val Val  
420 425 430

His Lys Lys Met Arg Pro Thr Ile Lys Asp His Trp Leu Lys His Pro  
435 440 445

Gly Leu Ala Gln Leu Cys Val Thr Ile Glu Glu Cys Trp Asp His Asp  
450 455 460

Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Glu Glu Arg Val Ser Leu  
465 470 475 480

Ile Arg Arg Ser Val Asn Gly Thr Thr Ser Asp Cys Leu Val Ser Leu  
485 490 495

Val Thr Ser Val Thr Asn Val Asp Leu Pro Pro Lys Glu Ser Ser Ile  
500 505 510

<210> 2  
<211> 375  
<212> PRT  
<213> Human

<400> 2

Met Gln Lys Leu Gln Leu Cys Val Tyr Ile Tyr Leu Phe Met Leu Ile  
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Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn  
20 25 30

Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr  
35 40 45

Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu  
50 55 60

Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Val Ile Arg Gln Leu  
65 70 75 80

Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val  
85 90 95

Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His  
100 105 110

Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu  
115 120 125

Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser  
130 135 140

Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu  
145 150 155 160

Arg Pro Val Glu Thr Pro Thr Val Phe Val Gln Ile Leu Arg Leu  
165 170 175

Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu  
180 185 190

Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val  
195 200 205

Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly  
210 215 220

Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr  
225 230 235 240

Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys  
245 250 255

Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys  
260 265 270

Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val  
275 280 285

Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr  
290 295 300

Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys  
305 310 315 320

Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala  
325 330 335

Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr  
340 345 350

Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val  
355 360 365

Val Asp Arg Cys Gly Cys Ser  
370 375

<210> 3  
<211> 378  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Chimera/Fusion

<400> 3

Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile  
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Ser Tyr Ile Tyr Ala Thr Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu  
20 25 30

Cys Ile Tyr Tyr Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser  
35 40 45

Gly Leu Glu Arg Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr  
50 55 60

Ala Ser Trp Arg Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly  
65 70 75 80

Cys Trp Leu Asp Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala  
85 90 95

Thr Glu Glu Asn Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe  
100 105 110

Cys Asn Glu Arg Phe Thr His Leu Pro Glu Ala Gly Gly Pro Glu Val  
115 120 125

Thr Tyr Glu Pro Pro Pro Thr Ala Pro Thr Gly Gly Arg Gly Asp Asp  
130 135 140

Asp Asp Lys Thr Arg Ser Arg Asp Lys Thr His Thr Cys Pro Pro Cys  
145 150 155 160

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
165 170 175

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
180 185 190

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
195 200 205

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu  
210 215 220

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu  
225 230 235 240

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
245 250 255

Lys Ala Leu Pro Val Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
260 265 270

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu  
275 280 285

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
290 295 300

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
305 310 315 320

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
325 330 335

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
340 345 350

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
355 360 365

Gln Lys Ser Leu Ser Leu Ser Pro Pro Lys  
370 375

<210> 4

<211> 1134

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimera/Fusion

<400> 4

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gcgactagt ggcgtgggga ggctgagaca cgggagtgc tctactacaa cgccaactgg 120

gagctggagc gcaccaacca gagcggcctg gagcgctgcg aaggcgagca ggacaagcgg 180

ctgcactgct acgcctcctg ggcacacgc tctggcacca tcgagctcgt gaagaagggc 240

tgctggctag atgacttcaa ctgctacgtt aggcaggagt gtgtggccac tgaggagaac 300

ccccaggtgt acttctgctg ctgtgaaggc aacttctgca acgagcgctt cactcatttg 360

ccagaggctg ggggccccgga agtcacgtac gagccacccc cgacagcccc caccggcggc 420

cgcggagacg acgacgacaa gacgcgttct agagacaaaa ctcacacatg cccaccgtgc 480

ccagcacctg aactcctggg gggaccgtca gtcttcctct tccccccaaa acccaaggac 540

accctcatga tctcccgac ccctgaggac acatgcgtgg tggggacgt gagccacgaa 600

gaccctgagg tcaagttcaa ctggtaacgtg gacggcgtgg aggtgcataa tgccaagaca 660

aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 720

caccaggact ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca 780

gtccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 840

accctgcccc	catccggga	ggagatgacc	aagaaccagg	tcagcctgac	ctgcctggtc	900
aaaggcttct	atcccagcga	catcgccgtg	gagtgggaga	gcaatggca	gccggagaac	960
aactacaaga	ccacgcctcc	cgtgctggac	tccgacggct	ccttcttct	ctatagcaag	1020
ctcaccgtgg	acaagagcag	gtggcagcag	gggaacgtct	tctcatgctc	cgtgatgcat	1080
gaggctctgc	acaaccacta	cacgcagaag	agcctctccc	tgtccccgcc	taaa	1134

<210> 5  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Linking Sequence, Gly-Ser repeat

<400> 5

Gly Ser Gly Ser  
1

<210> 6  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Linking Sequence, Enterokinase Cleavage Site

<400> 6

Asp Asp Asp Lys  
1